

SEQUENCE LISTING

<110> Zoon, et al.
 <120> Interferon Alpha Hybrids
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 <140> US 09/744,754
 <141> 2001-01-24
 <150> US 60/094,407
 <151> 1998-07-28
 <150> PCT/US99/15284
 <151> 1999-07-06
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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac	96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp	
20 25 30	
aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc	144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe	
35 40 45	
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc	192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr	
50 55 60	
ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc	240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr	
65 70 75 80	
ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg	288
Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu	
85 90 95	
gaa gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg	336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met	
100 105 110	
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act	384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr	
115 120 125	
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc	432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val	
130 135 140	
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa	480
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
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145 150 155 160

Ser Leu Arg Ser Lys Glu
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ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac	96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp	
20 25 30	
aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc	144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe	
35 40 45	
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc	192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr	
50 55 60	
ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc	240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser	
65 70 75 80	
ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc	288
Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu	
85 90 95	
gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg	336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met	
100 105 110	
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act	384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr	
115 120 125	
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gaa gtt gtc	432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val	
130 135 140	
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa	480
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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
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Ser Leu Arg Ser Lys Glu
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ctc ctg gca cag atg agg aga atc tct ctt ttc tcc tgc ttg aag gac	96
Leu Leu Ala Gln Met Arg Arg Ile Ser Leu Phe Ser Cys Leu Lys Asp	
20 25 30	

aga cgt gac ttt gga ttt ccc cag gag gag ttt ggc aac cag ttc caa	144
Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln	
35 40 45	

aag gct gaa acc atc cct gtc ctc cat gag atg atc cag cag atc ttc	192
Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe	
50 55 60	

aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc ctc	240
Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu	
65 70 75 80	

cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctc gag	288
Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu	
85 90 95	

gcc tgc gtg ata cag gag gtt ggg gtg gaa gag act ccc ctg atg aat	336
Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn	
100 105 110	

gtg gac tcc atc ctg gct gtg aag aaa tac ttc caa aga atc act ctt	384
Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu	
115 120 125	

tat ctg aca gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc aga	432
Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg	
130 135 140	

gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa aga	480
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Arg Arg Asp Phe Gly Phe Pro Gln Glu Glu Phe Gly Asn Gln Phe Gln
35 40 45

Lys Ala Glu Thr Ile Pro Val Leu His Glu Met Ile Gln Gln Ile Phe
50 55 60

Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr Leu
65 70 75 80

Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu Glu
85 90 95

Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met Asn
100 105 110

Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr Leu
115 120 125

Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val Arg
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Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu Arg
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Leu Arg Arg Lys Glu
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 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
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 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80
 ctc cta gaa aaa ttt tcc act gaa ctt aac cag cag ctg aat gac ctc 288
 Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
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 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
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 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu

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Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
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 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
 65 70 75 80
 ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctc 288
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
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 Ser Leu Arg Ser Lys Glu

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20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
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Ser Leu Arg Ser Lys Glu
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 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc caa gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
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 65 70 75 80
 ctc cta gac aaa ttc tac act gaa ctc tac cag cag ctg aat gac ctg 288
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
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 Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
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 aat gtg gac tcc atc ttg gct gtg aag aaa tac ttc caa aga atc act 384
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 Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tcc ttc tct tta tca aaa att ttt caa gaa 480
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 Arg Leu Arg Arg Lys Glu

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<210> 34
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Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
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Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Glu Val Gly Val Glu Glu Thr Pro Leu Met
100 105 110

Asn Val Asp Ser Ile Leu Ala Val Lys Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Thr Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Lys Ile Phe Gln Glu
145 150 155 160

Arg Leu Arg Arg Lys Glu
165

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 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80
 ctc cta gaa aaa ttt tac act gaa ctt aac cag cag ctg aat gac ctc 288
 Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160
 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu

165

<210> 36
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 36

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 37
 <211> 500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<220>
 <221> CDS
 <222> (1)..(498)
 <223>

<400> 37
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct gct tgg gat gag acc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
 65 70 75 80
 ctc cta gaa aaa ttt tcc act gaa ctt tac cag cag ctg aat gac ctc 288
 Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160
 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu

165

<210> 38
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 38

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Ala Trp Asp Glu Thr
65 70 75 80

Leu Leu Glu Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 39
 <211> 500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<220>
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 <223>

<400> 39	
tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata	48
Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile	
1 5 10 15	
ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac	96
Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp	
20 25 30	
aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc	144
Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe	
35 40 45	
cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc	192
Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr	
50 55 60	
ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc	240
Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser	
65 70 75 80	
ctc cta gac aaa ttc tcc act gaa ctc tac cag cag ctg aat gac ctc	288
Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu	
85 90 95	
gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg	336
Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met	
100 105 110	
aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act	384
Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr	
115 120 125	
ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc	432
Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val	
130 135 140	
aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa	480
Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu	
145 150 155 160	
agt tta aga agt aag gaa tg	500
Ser Leu Arg Ser Lys Glu	

165

<210> 40
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 40

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Asp Lys Phe Ser Thr Glu Leu Tyr Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165

<210> 41
 <211> 500
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> Gene Fusion

<220>
 <221> CDS
 <222> (1)..(498)
 <223>

<400> 41
 tgt gat ctg cct cag acc cac agc ctg ggt aat agg agg gcc ttg ata 48
 Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
 1 5 10 15
 ctc ctg gca caa atg gga aga atc tct cct ttc tcc tgc ctg aag gac 96
 Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
 20 25 30
 aga cat gac ttt gga ttc ccc cag gag gag ttt gat ggc aac cag ttc 144
 Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
 35 40 45
 cag aag gct caa gcc atc tct gtc ctc cat gag atg atc cag cag acc 192
 Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
 50 55 60
 ttc aat ctc ttc agc aca aag gac tca tct gct act tgg gaa cag agc 240
 Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
 65 70 75 80
 ctc cta gac aaa ttc tac act gaa ctc aac cag cag ctg aat gac ctc 288
 Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
 85 90 95
 gag gcc tgt gtg ata cag ggg gtg ggg gtg aca gag act ccc ctg atg 336
 Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
 100 105 110
 aag gag gac tcc att ctg gct gtg agg aaa tac ttc caa aga atc act 384
 Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
 115 120 125
 ctc tat ctg aaa gag aag aaa tac agc cct tgt gcc tgg gag gtt gtc 432
 Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
 130 135 140
 aga gca gaa atc atg aga tct ttt tct ttg tca aca aac ttg caa gaa 480
 Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
 145 150 155 160
 agt tta aga agt aag gaa tg 500
 Ser Leu Arg Ser Lys Glu

165

<210> 42
<211> 166
<212> PRT
<213> Artificial Sequence

<220>
<223> Gene Fusion

<400> 42

Cys Asp Leu Pro Gln Thr His Ser Leu Gly Asn Arg Arg Ala Leu Ile
1 5 10 15

Leu Leu Ala Gln Met Gly Arg Ile Ser Pro Phe Ser Cys Leu Lys Asp
20 25 30

Arg His Asp Phe Gly Phe Pro Gln Glu Glu Phe Asp Gly Asn Gln Phe
35 40 45

Gln Lys Ala Gln Ala Ile Ser Val Leu His Glu Met Ile Gln Gln Thr
50 55 60

Phe Asn Leu Phe Ser Thr Lys Asp Ser Ser Ala Thr Trp Glu Gln Ser
65 70 75 80

Leu Leu Asp Lys Phe Tyr Thr Glu Leu Asn Gln Gln Leu Asn Asp Leu
85 90 95

Glu Ala Cys Val Ile Gln Gly Val Gly Val Thr Glu Thr Pro Leu Met
100 105 110

Lys Glu Asp Ser Ile Leu Ala Val Arg Lys Tyr Phe Gln Arg Ile Thr
115 120 125

Leu Tyr Leu Lys Glu Lys Lys Tyr Ser Pro Cys Ala Trp Glu Val Val
130 135 140

Arg Ala Glu Ile Met Arg Ser Phe Ser Leu Ser Thr Asn Leu Gln Glu
145 150 155 160

Ser Leu Arg Ser Lys Glu
165